BLASTN 2.2.1 [Apr-13-2001]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Sch?ffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1009527356-10099-15388

Query=
(1440 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences).
1,073,652 sequences; 4,829,212,789 total letters

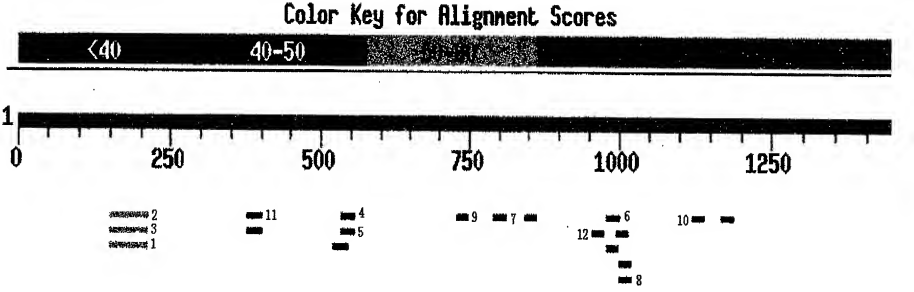
If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 19 Blast Hits on the Query Sequence

	Sequences producing significant alignments:	Score (bits)	E Value
1	gi|9628890|ref|NC_001723.1| Peanut stripe virus, complete g...	68	2e-08
2	gi|1016234|gb|U34972.1|PSU34972 Peanut stripe virus mRNA po...	68	2e-08
3	gi|1335723|gb|U05771.1|PSU05771 Peanut stripe virus, comple...	68	2e-08
4	gi|15642775|ref|NC_000853.1| Thermotoga maritima, complete ...	44	0.36
5	gi|4980775|gb|AE001710.1|AE001710 Thermotoga maritima secti...	44	0.36
6	gi|16973823|emb|AL354976.11|AL354976 Human DNA sequence fro...	42	1.4
7	gi|7838255|emb|AL132822.15|HSJ1017F8 Human DNA sequence fro...	42	1.4
8	gi|15341592|gb|AC018499.3| Homo sapiens chromosome 3 clone ...	40	5.6
9	gi|14589685|gb|AC008167.5| Homo sapiens BAC clone RP11-1720...	40	5.6
10	gi|16445165|gb|AC092038.3| Homo sapiens chromosome 3 clone ...	40	5.6
11	gi|15020311|gb|AY040316.1| Hylurdrectonus araucariae elonga...	40	5.6
12	gi|14670056|gb|AC073614.17|AC073614 Homo sapiens Xp BAC RP1...	40	5.6

Fig.1a



Sequence	Alignment Score
1-3	50-80
4-12	40-50

Fig.1b

BLASTN 2.2.1 [Apr-13-2001]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Sch?ffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1010120805-18751-22816

Query=
(882 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences).
1,079,316 sequences; 4,832,507,720 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 143 Blast Hits on the Query Sequence

Fig.2a

2015220-3265-0015-0001

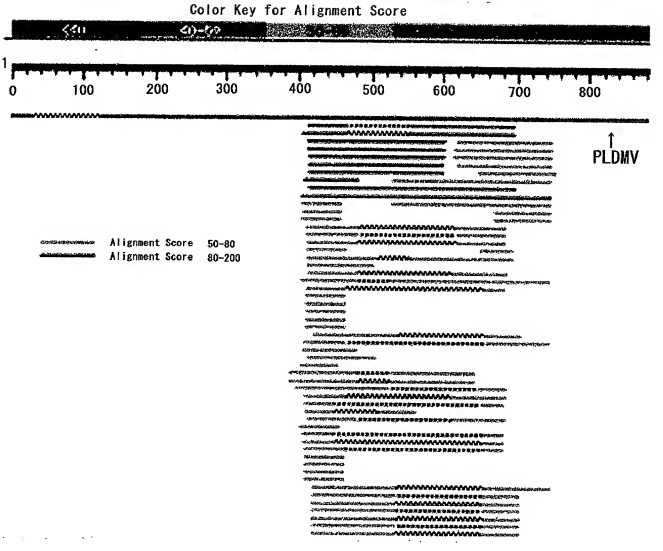


Fig.2b

BLASTN 2.2.1 [Apr-13-2001]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Sch?ffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1010127418-14473-18661

Query=
(1374 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences).
1,079,316 sequences; 4,832,507,720 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 99 Blast Hits on the Query Sequence

Fig.3a

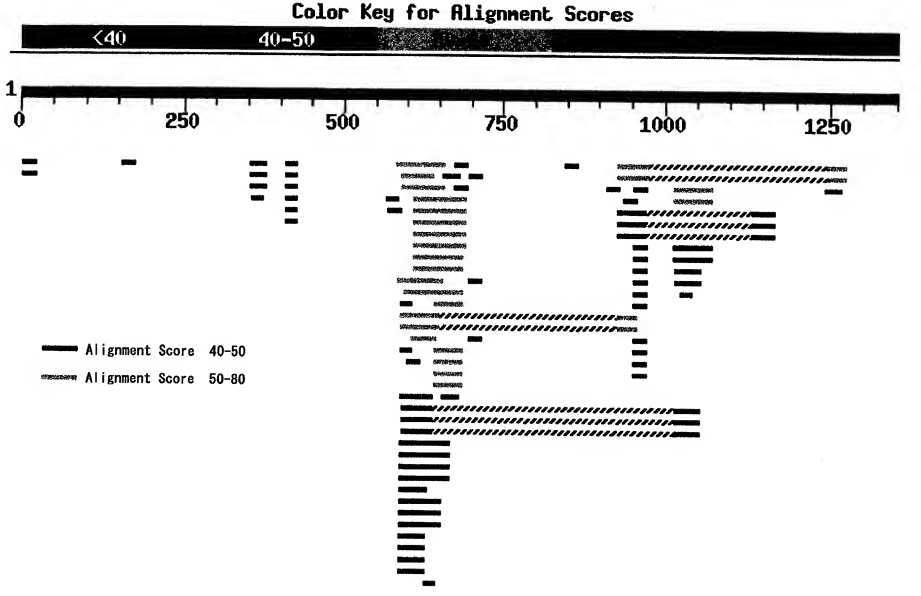

Color Key for Alignment Scores
<40
40-50
1
0
250
500
750
1000
1250
Alignment Score 40-50
Alignment Score 50-80

Fig.3b

BLASTN 2.2.1 [Apr-13-2001]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Sch?ffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1010128690-26317-13567

Query=
(1563 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences).
1,079,316 sequences; 4,832,507,720 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 175 Blast Hits on the Query Sequence

Fig.4a

20120-0393.001

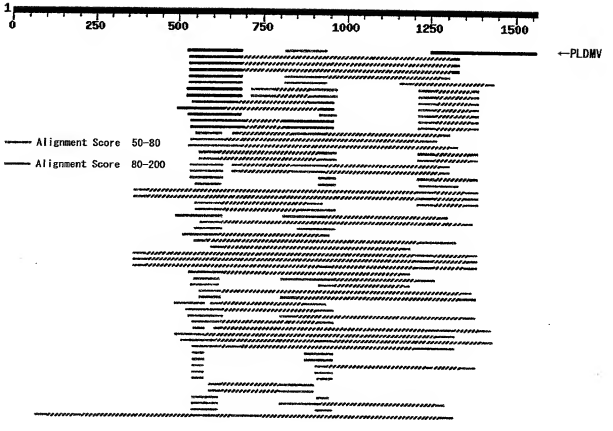


Fig.4b